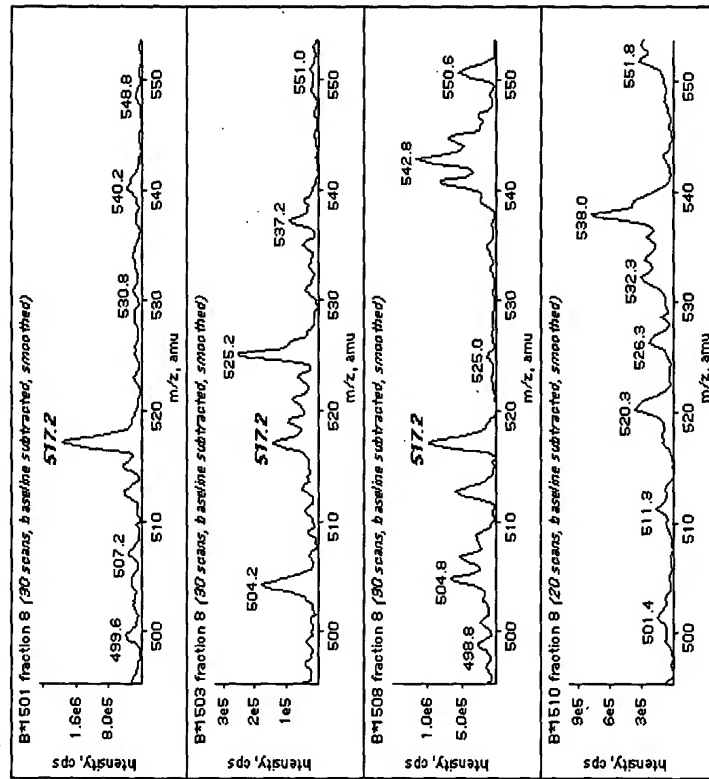


A



C

y-ions: 9 8 7 6 5 4 3 2 1 (SEQ ID NO:138)
 1033 919 791 663 526 469 382 311 182
 N Q Z H G S A E Y
 115 243 371 508 565 652 723 852 1015
 b-ions: 1 2 3 4 5 6 7 8 9

B

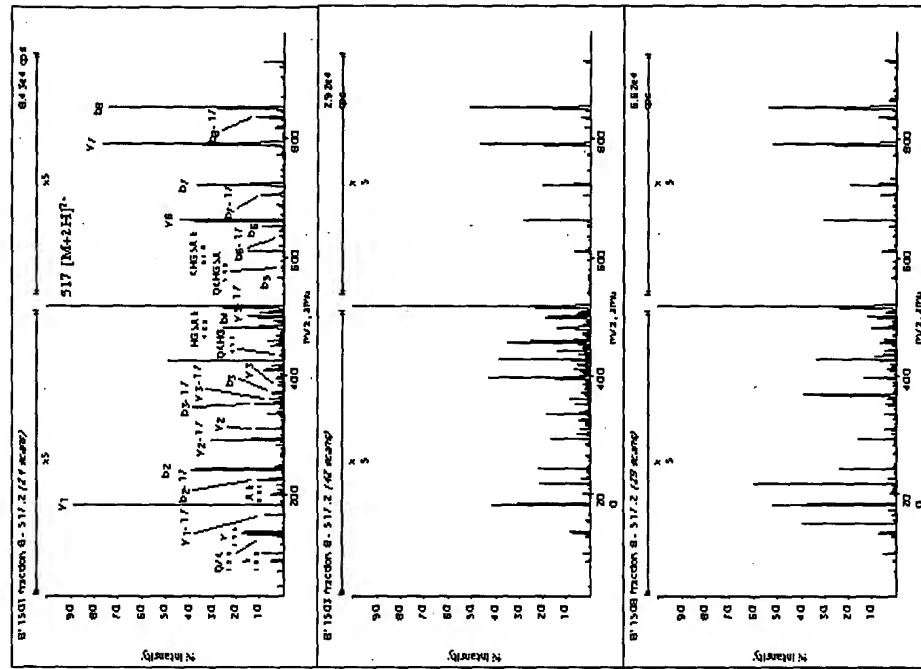
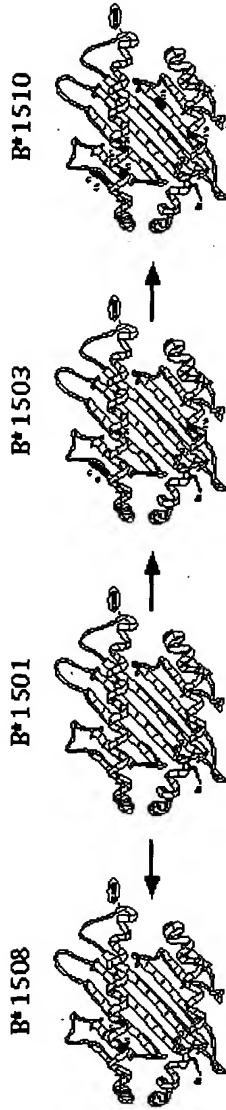


FIG. 13



100022066 . 090902



SEQ ID NO:

134
--MDRHTXF
-----YT
GSHFGVAY
TG-----AY
FVSMRAY
SOFDRVTV
XAN---VT
FLZAMZSTY
TVXDSITHY
VVACV---Y
PLA-N-HTV
VVAPITGY
FOARETEY
VEVVDIOF
---XVE
TENVXSEY
AATCG---XV
TAN---ET
ILGPFSSY
ALGDVNH
YMLPSGVSY

SEQ ID NO:

138
NQZMGSAEY
TPXGEPIZSY
SQFGGSGY
CPLSCFT

SEQ ID NO:

135
ACFASGAGZ
-G---CDV
APMARGZY
GQIZAVDF
NPFAZZN
-Q-DEPPDMZY
GQVAGGSVF
AEFNACZY

FIG. 26



B*1508



B*1501



B*1503



FIG. 27

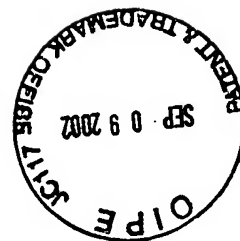
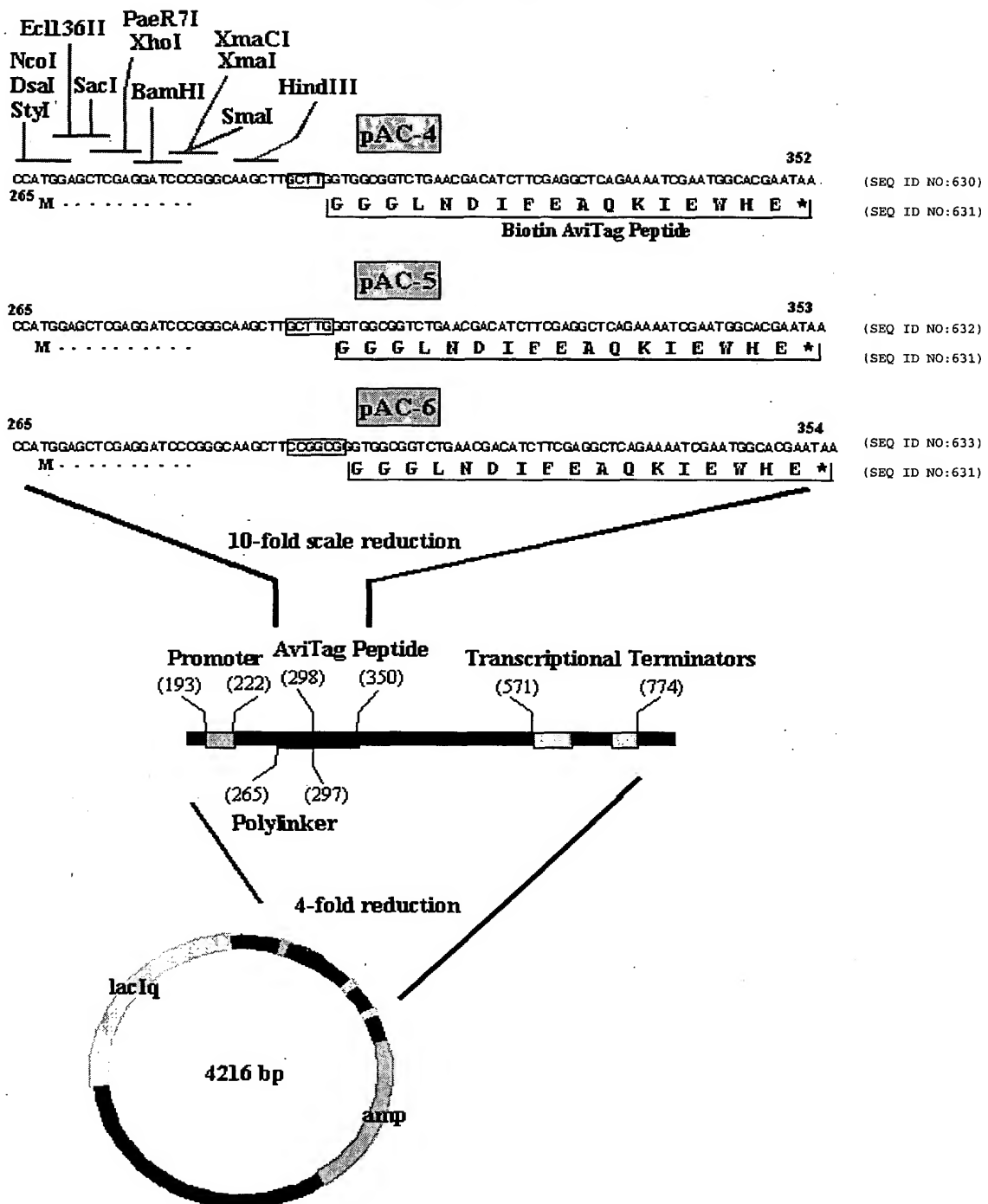
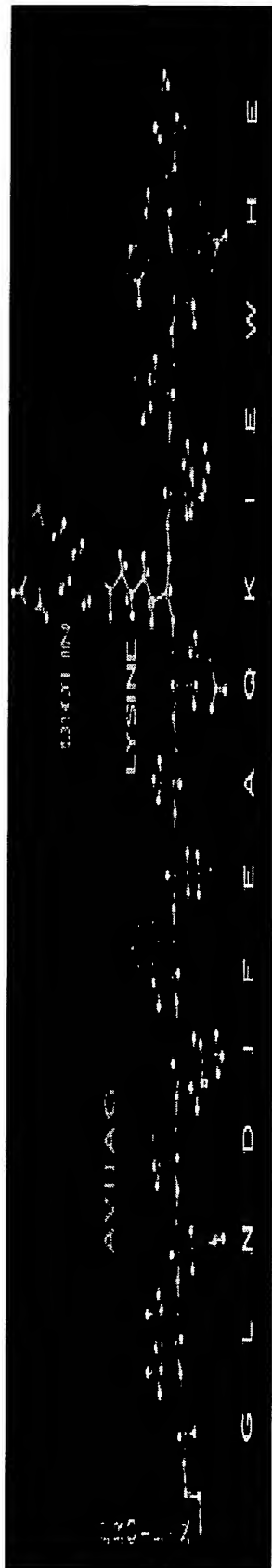


FIG. 41





(residues 3 to 17 of SEQ ID NO:631)

FIG. 42



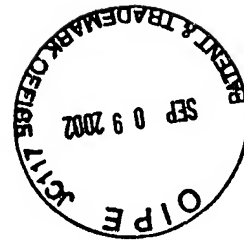
consensus	24	45	46	63	67	116	156	166	167	ethnicity	SEQ ID NO:
	A	M	A	E	S	S	W	E	W		
B*1512	-	-	-	-	-	-	-	D	G	Thai	1
B*1508	-	-	-	N	F	-	-	-	-	Iranian/Indian/Amerindian	2
B*1501	-	-	-	-	-	-	-	-	-	Caucasian	3
B*1503	S	E	E	-	-	-	L	-	-	Black	4
B*1518	S	E	E	N	C	-	L	-	-	Indian	5
B*1510	S	E	E	N	C	Y	L	-	-	Black	6
											7

TABLE 1

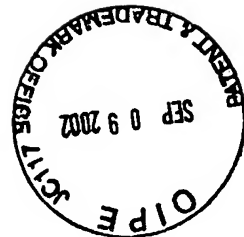


Primer	type	sequence (5'→3')	SEQ ID NO:
HLA5UT	PCR (5'; inserts <i>Sall</i> site)	GGGCTCGACGGACTCAGAAATCTCCCCAGACGCCGAG	8
sHLA3TM	PCR (3'; inserts stop codon and <i>HindIII</i> site)	CCGCAAGCTTTCATCTCAGGGTGAG	9
5PXI	PCR (5'; inserts <i>XbaI</i> site)	GGGCTCTAGAGGACTCAGAAATCTCCCCAGACGCCGAG	10
3PEI	PCR (3'; inserts stop codon and <i>EcoRI</i> site)	CCGCGAATTTCATCTCAGGGTGAG	11
M13 universal	sequencing (mp18, end through α_1) (mp19, leader through α_2)	TGTAAACGACGGCCAGT	12
3S	sequencing (α_2 through α_1)	CGGCAAGGATTACATCGCCCTG	13
JD3S	sequencing (α_3 through end)	CCCCATCGTGGGCATCGTTG	14
3N	sequencing (α_2 through leader)	CAGGGCGATGTAATCCTTGCCG	15
4N	sequencing (α_3 through α_2)	GCCAGGTCAGTGTGATCTCCGC	16
T7 promoter	sequencing (T7 promoter forward priming site)	TAATACGACTCACTATAGGG	17
pcDNA3.1/BGH	sequencing (BGH reverse priming site)	TAGAAGGCACAGTCGAGG	18

TABLE 2



10022066 - 090902



206060 - 99022001

allele	# fractions	P2 extras	P9 extras	>9 cycles?
B*1501	7	P	-	yes (14)
B*1508	8	QVKRS (SEQ ID NO:19)	IVMQ (SEQ ID NO:20)	yes (14)
B*1503	3	P	MNL	yes (14)
B*1510	3	PR	MIY	yes (14)

TABLE 3



10022066 .090902

SEQ ID NO:	ligand	source protein	allele(s) characterized from
<i>HLA ligands</i>			
21	VGYYDDTQF	HLA-I α (49-57)	B*1501, 1508
22	IAYGYVDDTQF	HLA-I α (47-57)	B*1501, B*1512
23	IKADHVSTY	HLA-II DP α (32-40)	B*1503
24	GSHSMRYF	HLA-I α (25-32)	B*1503
<i>Replication/transcription/translation ligands</i>			
25	GQRKGAGSVF	60S ribosomal protein L8 (7-16)	B*1501, 1503
26	AQAESLRY	40S ribosomal protein S3 (100-107)	B*1501
27	GKVRTDITY	40S ribosomal protein S4 (73-81)	B*1503
28	SHAQTVVL	40S ribosomal protein S27 (48-55)	B*1510
29	SQFGGGSQY	eIF3-p66 (61-69)	B*1501, 1503, 1508, B*1512
30	VQGPVGTDF	zinc finger transcription factor (296-304)	B*1501
31	APPPPPPP	transcription factor ZFM1 (581-589)	B*1501
32	YQHTGAVL	spleen mitotic checkpoint BUB3 (53-60)	B*1510
33	AHGRKMSKSL	valyl-tRNA synthetase (859-868)	B*1510
34	LPHQPLATY	Oct-binding factor 1 (52-60)	B*1508
35	AKYSTPATL	probable ATP-dependent RNA helicase DDX10 (280-288)	B*1503
36	AKAGITTTT	DNA replication licensing factor MCM5 (470-478)	B*1503
37	TQAPGNPVL	splicing factor U2AF large chain (179-187)	B*1510
38	SHQRQLLL	Kin17 (49-56)	B*1510
39	NQFQALLQY	polypyrimidine tract-binding protein (220-228)	B*1512
<i>Biosynthetic/degradative modification ligands</i>			
40	FVSNHAY	aldolase A (358-364)	B*1501, 1508
41	ILGPPGSVY	ubiquitin-protein ligase (83-91)	B*1501, B*1502, 1508, B*1512
42	YMIDPSGVSY	proteasome subunit C8 (150-159)	B*1501, B*1502, 1508, B*4601, B*1512
43	NHAIVSTSV	26S protease (S4) regulatory subunit (741-749)	B*1510
44	IHTPENPVI	lanosterol 14- α demethylase (488-496)	B*1510

TABLE 4



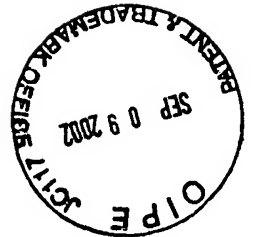
10022066 .090902

45	AHSNLASVL	O-linked GlcNAc transferase (237-245)	B*1510
Signalling/modulatory ligands			
46	VVAPITTTY	calcyclin binding protein (63-71)	B*1501, 1508
47	GHSPPTSSL	tyrosine-protein kinase JAK3 (491-499)	B*1510
48	LPPPPPPPP	Fas antigen ligand (54-62)	B*1503
49	NHANGTL	serine/threonine protein phosphatase PP2A (α and β) (229-236)	B*1510
Transporter/chaperone ligands			
50	EHVASSPAL	13S Golgi transport complex 90 kD subunit (741-749)	B*1510
51	HHSDGSVSL	tapasin (354-362)	B*1509, B*1510
52	QPGPQIVY	GABA/noradrenaline transporter (261-268)	B*1503
Structural/cytokinesis ligands			
53	NMNDLVSEY	tubulin β chain (414-422)	B*1508
54	THTQPGVQL	sepin 2 homolog (70-78)	B*1509, B*1510
55	SHANSVVL	β -adaptin (249-257)	B*1509, B*1510
Unknown function ligands			
56	GQYPTQPTY	KIAA0058 (5-13); like <i>Mus musculus</i> proline-rich protein	B*1503
57	VKVIQQESY	mammary tumor-associated protein INT6 (278-286)	B*1503
58	AKYPHVEDY	Ki nuclear autoantigen (207-215)	B*1503
59	AMNPTNTVF	heat shock cognate 71 kD protein (60-68)	B*1503
60	CPLSCFT	human HTGS database	B*1501, B*1503, B*1508
61	MPHSGYGF	human EST	B*1508
62	CHSAFAL	human HTGS database	B*1510
63	LHLLTLEA	human EST	B*1510
64	KNANLVQLY	human EST	B*1512

TABLE 4 CONT'D.

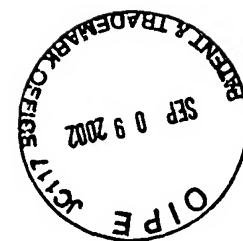
fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
7	504.1 (+2)	H M S G Z P T S Y	65
7	549.2 (+2)	H N Z A A H Z E Y	66
8	526.0 (+2)	H A A X Y S Z V Y	67
10	484.3 (+2)	Y Q S D H R Y	68
11	424.3 (+2)	H X S T Z D F	69
11	464.3 (+2)	H A P P T D P P P	70
11	550.0 (+2)	H G P A N R D S V F	71
11	563.3 (+2)	F P Y P T D P Z Y	72
12	531.2 (+2)	Z N A N X V Z X Y	73
14	585.6 (+2)	R S F X X E N E Y	74
16	488.7 (+2)	H M Z N P T S Y	75
16	661.9 (+2)	Y V X F - - - V Y	76
17	577.6 (+2)	R S M X R C P E Y	77
18	523.0 (+2)	- - F V T A Z T Y	78
20	582.4 (+2)	M Y N C N E X D Y	79
25	562.8 (+2)	N Q F Q A L L Q Y	80

TABLE 5



ALLELE	7	9	24	25	26	34	35	36	45	62	63	66	67	70	99	159	163	167	SEQ ID NO:	P2 MOTIF
consensus	Y	Y	A	V	G	V	R	F	M	R	E	I	S	N	Y	Y	L	W		(dominant/strong)
B*1508	-	-	-	-	-	-	-	-	-	-	N	-	F	-	-	-	-	-	81	PA
B*1513	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	83	ILQVP (SEQ ID NO:126)
B*1502	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	84	LVQP (SEQ ID NO:163)
B*1501	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	85	QMLV (SEQ ID NO:529)
B*1512	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	86	QLM
B*1503	-	-	S	-	-	-	-	-	E	-	-	-	-	-	-	-	-	-	87	QKM
B*1518	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	88	H
B*1509	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	89	H
B*1510	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	90	H
B*1517	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	91	TS
B*1516	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	92	T
B*4601	-	-	-	-	-	-	-	-	-	-	-	K	Y	Q	-	-	-	-	93	MI

Table 6



[illegible]

TABLE 7



10022066.090902

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
9	490.3 (+2)	A G G Z P A T P P A X	107
9	513.1 (+2)	S H Z G C V Z P A V	108
10	433.8 (+2)	G H D P D S P A A	109
10	455.4 (+2)	E H V A S S P A L	110
10	482.6 (+2)	M C Z - G M P A X	111
10	482.8 (+2)	G H G A N N D P A X	112
10	495.7 (+2)	X H S Z P A G P A X	113
11	448.9 (+2)	M H A D N P V X	114
11	482.8 (+2)	G H <u>C</u> <u>P</u> R N P A X	115
11	495.7 (+2)	X H S G A P Z A P X	116
11	516.7 (+2)	X H D <u>T</u> <u>E</u> <u>H</u> <u>A</u> P X	117
12	448.4 (+2)	T Q A P G N P V L	118
12	460.3 (+2)	T Z A <u>G</u> <u>C</u> <u>M</u> <u>V</u> P X	119
13	464.8 (+2)	M V - - H P V X	120
14	456.7 (+2)	A H S V P S P A F	121
14	477.7 (+2)	M H T - - P A P V	122
14	482.8 (+2)	P G A A V V P S X	123
15	510.1 (+2)	I H T P E N P V I	124
16	456.7 (+2)	S H <u>D</u> <u>G</u> <u>S</u> V P T X	125
16	522.7 (+2)	- - - - - P V X	N/A
16	523.3 (+2)	M A H S - - P V F	127
17	523.2 (+2)	- H - - - - P V F	128
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X	129
18	491.2 (+2)	V H T C V N P V X	130
18	515.8 (+2)	E W <u>H</u> <u>Y</u> P V S X	131
19	496.6 (+2)	<u>E</u> <u>T</u> <u>P</u> <u>E</u> H A P V X	132

TABLE 8

side chain (SEQ ID NO:133)	P1	P2	P3	P4	C ¹	C ²	C ³	C ⁴	C ⁵	side chain (SEQ ID NO:133)
G	-	-	11.90%	10.32%	11.90%	-	-	-	-	G
P	-	10.32%	-	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	-	C
A	18.25%	11.11%	11.90%	-	-	-	-	10.32%	-	A
V	11.90%	-	-	-	-	10.32%	-	-	-	V
F	-	-	-	-	-	-	-	26.19%	-	F
M	-	-	-	-	-	-	-	-	-	M
I/L	13.49%	13.49%	-	-	-	-	-	-	-	I/L
S	-	-	-	-	-	-	-	-	-	S
T	-	-	-	-	-	13.49%	-	-	-	T
Y	-	-	-	-	-	-	-	63.49%	-	Y
N	-	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	-	W
Q/K	-	24.60%	-	-	-	-	-	15.87%	-	Q/K
H	-	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	10.32%	-	E
N value	13.64	19.52	3.80	0.32	1.90	3.81	6.51	69.68	C value	
N _{sum}	37.28				81.90					C _{sum}
					B*1501 N _{sum} /C _{sum} = 0.46					

$$B * 1501 \text{ } N_{\text{sum}} / C_{\text{sum}} = 0.46$$

TABLE 9



side chain (SEQ ID NO:133)	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain (SEQ ID NO:133)
G	12.16%	-	12.16%	13.51%	12.16%	-	-	-	G
P	-	10.81%	-	12.16%	10.81%	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	31.08%	-	-	-	-	-	-	-	A
V	-	-	-	-	-	-	-	-	V
F	-	-	-	-	-	-	-	20.27%	F
M	-	-	-	-	-	-	-	-	M
I/L	-	-	-	-	-	13.51%	-	-	I/L
S	-	-	-	-	-	10.81%	-	-	S
T	-	-	-	-	-	13.51%	17.57%	-	T
Y	-	-	-	-	-	-	-	68.92%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	43.24%	-	-	13.51%	12.16%	14.86%	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	23.24	34.05	2.16	5.67	6.48	9.99	12.43	69.19	C value
N _{sum}	65.12				98.09				C _{sum}
B*1503 N _{sum} /C _{sum} = 0.66									



TABLE 10

side chain (SEQ ID NO:133)	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain (SEQ ID NO:133)
G	-	-	-	-	10.42%	-	-	-	G
P	-	27.08%	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	16.67%	13.54%	-	-	-	14.58%	-	A
V	-	-	-	-	-	11.46%	12.50%	-	V
F	-	-	-	-	-	-	-	23.96%	F
M	-	-	-	-	-	-	-	-	M
I/L	11.46%	-	-	-	-	-	-	-	I/L
S	-	-	-	-	-	11.46%	11.46%	-	S
T	10.42%	-	-	-	-	-	17.71%	-	T
Y	11.46%	-	-	-	-	-	-	66.67%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	12.50%	-	-	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	10.42%	-	E
N value	3.34	23.75	3.54	0.00	2.92	2.92	16.67	70.63	C value
N _{sum}	30.63				93.14				C _{sum}

$$B * 1508 \text{ N}_{\text{sum}} / C_{\text{sum}} = 0.33$$



TABLE 11



10022066 . 090902

side chain (SEQ ID NO:133)	P1	P2	P3	P4	C ³	C ²	C ¹	C-t m	side chain (SEQ ID NO:133)
G	10.57%	-	10.57%	10.57%	11.38%	-	-	-	G
P	-	-	-	12.20%	-	28.46%	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	-	19.51%	-	-	-	14.63%	-	A
V	-	-	-	-	-	-	22.76%	10.57%	V
F	-	-	-	-	-	-	-	-	F
M	11.38%	-	-	-	-	-	-	-	M
I/L	12.20%	-	-	-	-	-	12.20%	70.73%	I/L
S	11.38%	-	-	-	-	-	15.45%	-	S
T	-	-	-	-	-	-	-	-	T
Y	-	-	-	-	-	-	-	-	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	-	-	-	-	Q/K
H	-	58.54%	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	5.53	48.54	10.08	2.77	1.38	18.46	25.04	61.3	C value
N _{sum}	66.92				106.18				C _{sum}

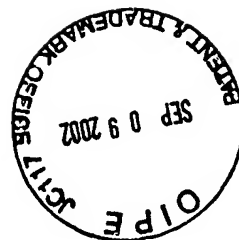
$B * 1510 \text{ N}_{\text{sum}} / C_{\text{sum}} = 0.63$

TABLE 12

side chain (SEQ ID NO: 133)	P1	P2	P3	P4	C ³	C ²	C ¹	C-term	side chain (SEQ ID NO: 133)
G	-	-	-	-	-	-	-	-	G
P	-	-	-	13.33%	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	16.67%	-	13.33%	-	-	-	-	A
V	-	-	-	-	-	-	16.67%	-	V
F	-	-	16.67%	-	-	-	-	16.67%	F
M	-	13.33%	-	-	-	-	-	-	M
IL	-	13.33%	13.33%	16.67%	-	-	-	-	IL
S	-	-	-	-	-	13.33%	-	-	S
T	-	-	-	-	-	13.33%	-	-	T
Y	13.33%	-	-	-	-	-	-	80.00%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	16.67%	13.33%	-	-	20.00%	13.33%	-	Q/K
H	23.33%	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	13.33%	16.67%	-	-	-	D
E	-	-	-	-	-	-	16.67%	-	E
N value	16.66	20.00	13.33	16.66	6.67	16.66	16.67	76.67	C value
N _{sum}	66.65				116.67				C _{sum}

$$B * 1512 \text{ N}_{\text{sum}} / C_{\text{sum}} = 0.57$$

TABLE 13



Fract ion	Ion for MS/MS	derived peptide sequence	SEQ ID NO:	alleles overlapping
6	398.2 (+3)	- - W D R H T X F	134	B*1501/B*1508
6	448.2 (+2)	- - - - - Y T	N/A	B*1501/B*1508
7	418.7 (+2)	A Q F A S G A G Z	135	B*1501/B*1503
8	402.2 (+2)	- G - - C D Y	136	B*1501/B*1503
8	418.7 (+2)	G S H F G V A Y	137	B*1501/B*1508
8	516.7 (+2)	N Q Z H G S A E Y	138	B*1501/B*1503/B*1508 /B*1512
8	642.7 (+2)	P M N D W X M T Z T Y	139	B*1501/B*1512
9	331.4 (+3)	A P M A R G Z Y	140	B*1501/B*1503
9	418.7 (+2)	F V S N H A Y	141	B*1501/B*1508
9	433.2 (+2)	N P P A Z Z P N	142	B*1501/B*1503
9	437.0 (+2)	T G - - - A Y	143	B*1501/B*1508
9	441.2 (+2)	- Q - D P P P D M Z Y	144	B*1501/B*1503
9	446.6 (+2)	G Q Z Z A V D F	145	B*1501/B*1503
9/10	465.2 (+2)	S Q F G G G S Q Y	146	B*1501/B*1503/B*1508 /B*1512
9	476.2 (+2)	S Q F D H V T Y	147	B*1501/B*1508
9	578.0 (+2)	T P X G E P Y Z S Y	148	B*1501/B*1503/B*1508
10	398.3 (+2)	X A N - - V T	149	B*1501/B*1508
10	456.8 (+2)	C P L S C F T	150	B*1501/B*1503/B*1508
10	509.0 (+2)	F L Z A M Z S T Y	151	B*1501/B*1508/B*1512
10	532.0 (+2)	T V X D S Z T H Y	152	B*1501/B*1508/B*1512
13	503.6 (+2)	G Q R K G A G S V F	153	B*1501/B*1503
14	460.7 (+2)	V V A P I T T G Y	154	B*1501/B*1508
14	475.1 (+2)	V V A C V - - Y	155	B*1501/B*1508
14	525.3 (+2)	P L A - N - H T Y	156	B*1501/B*1508
15	514.2 (+2)	F Q A R X T E Y	157	B*1501/B*1508
16	522.0 (+2)	V G Y V D D T Q F	158	B*1501/B*1508
17	351.3 (+3)	A A F C G - - X V	159	B*1501/B*1508
17	408.7 (+2)	Y L H - - E T	160	B*1501/B*1508
17/18	451.4 (+2)	I L G P P G S V Y	161	B*1501/B*1508/B*1512
17	462.4 (+2)	X L G D V N M Y	162	B*1501/B*1508
17	507.0 (+2)	- - - - X V E F	163	B*1501/B*1508
17	519.2 (+2)	T A R V X S V E Y	164	B*1501/B*1508
18	565.7 (+2)	A E F W A C Z X Y	165	B*1501/B*1503
18/19	566.2 (+2)	Y M I D P S G V S Y	166	B*1501/B*1508/B*1512
19/20	560.0 (+2)	X V E X T T D Y Y	167	B*1501/B*1512
20/21	448.2 (+2)	A A G X G P T F Y	168	B*1501/B*1512
20/21	614.0 (+2)	I A V G Y V D D T Q F	169	B*1501/B*1512
21/22	507.2 (+2)	V A F V X F V G Y	170	B*1501/B*1512
21/22	557.2 (+2)	Y N R W S X E F	171	B*1501/B*1512
22/23	510.8 (+2)	A L M P - - X N Y	172	B*1501/B*1512

TABLE 14



motif P2/P9		SEQ ID NO:	+ length variation only	SEQ ID NO:	+ P2 variation only	SEQ ID NO:
PLASMDRY (64-72)	173	MQLLCVF (1-7)	195	DIEGHASHY (28-36)	245	
MLNRYKLIY (68-76)	174	HLDIEGHASHY (26-36)	196	SAPLEKQLF (123-131)	246	
PLEKQLFY (125-133)	175	MLSAPLEKQLF (121-131)	197	APLEKQLFY (124-132)	247	
YQLRCHLSY (149-157)	176	PLEKQLF (125-131)	198	LPNTRPHSY (138-146)	248	
ALSINGDKF (159-167)	177	PLEKQLFY (125-132)	199	NTRPHSYVF (140-148)	249	
DLPDLRGPF (203-211)	178	TMLPNTRPHSY (136-146)	200	SINGDKFQY (161-169)	250	
FVPNLKDMF (242-250)	179	MLPNTRPHSY (137-146)	201	YTGAMTSKF (169-177)	251	
AVTMTAASY (253-261)	180	QLRCHLSY (150-157)	202	TSKFLMGTY (174-182)	252	
TMFEVSAF (290-298)	181	YVALSINGDKF (157-167)	203	LTSAQSGDY (216-224)	253	
DLRWLAKSF (314-322)	182	FQYTGAMTSKF (167-177)	204	YSLVIVTTF (224-232)	254	
HLTTEKQY (366-374)	183	AMTSKFLMGTY (172-182)	205	VIVTTFVHY (227-235)	255	
ALRLATVGY (375-383)	184	HVLSLVF (192-198)	206	TTFVHYANF (238-246)	256	
ALGTESGLF (467-475)	185	SLTSAQSGDY (215-224)	207	MTAASYARY (256-264)	257	
AVSNAVDGF (505-513)	186	SLVIVTTF (225-232)	208	DTETLTTF (284-292)	258	
ALYEASTTY (564-572)	187	LVIVTTF (226-232)	209	ATVKGMQSY (338-346)	259	
RQIPKIQNF (597-605)	188	IVTTFVHY (228-235)	210	ATSVLLSAY (396-404)	260	
ILSSNYFDF (643-651)	189	IVTTFVHYANF (228-238)	211	SAYNRHPLF (402-410)	261	
TVMEIAGLY (666-674)	190	FVHYANFHNF (232-241)	212	HTVMRETLF (414-422)	262	
HVVLAILLY (679-687)	191	FVHYANFHNFY (232-242)	213	ESGLFSPCY (471-479)	263	
VVLAILLYF (680-688)	192	TMTAASY (255-261)	214	SPCYLSLRF (476-484)	264	
FLVHKIVMF (696-704)	193	TMTAASYARY (255-264)	215	IIPLINVTF (544-552)	265	
LVHKIVMFF (697-705)	194	ELDTETLTTF (282-292)	216	TTYLSSSLF (570-578)	266	
		TMFEVSAFF (290-399)	217	NSILSSNYF (641-649)	267	
		TVLKDIIGICY (326-326)	218	AILLYFIAP (683-691)	268	
		VLKDIIGICY (327-326)	219	FIAFALGIF (688-696)	269	
		TVKGMQSY (339-346)	220			
		RLATVGY (377-383)	221			
		TVGYPKAGVY (380-389)	222			
		LLSAYNRHPLF (400-410)	223			
		PLHTVMRETLF (412-422)	224			
		VMRETLF (416-422)	225			
		GLALGTESGLF (465-475)	226			
		GLFSPCY (473-479)	227			
		LMIPLINVTF (542-552)	228			
		PLINVTF (546-552)	229			
		EVGRSALY (559-566)	230			
		YLSSSLF (572-578)	231			
		TQKSCIF (608-614)	232			
		TQKSCIFCGF (608-617)	233			
		GLET'TTY (627-633)	234			
		VQNSILSSNY (639-648)	235			
		VQNSILSSNYF (639-649)	236			
		ILSSNYF (643-649)	237			
		VMEIAGLY (667-674)	238			
		VVLAILLY (680-687)	239			
		VVLAILLYF (680-688)	240			
		VLAILLY (681-687)	241			
		VLAILLYF (681-688)	242			
		VLAILLYFIAP (681-691)	243			
		ILYFIAP (685-691)	244			
		FLVHKIVMFF (696-705)	245			

TABLE 16

TABLE 17

Primer name	Sequence 5'-3'	SEQ ID NO:	Locus	Cut site	Annealing site
PP5UTA	GCGCTCTAGACCCAGACGCCGAGGATGGCC	270	A	XbaI	5UT
3PP14A	GCCCTGACCCCTGCTAAAGGT	271	A		Intron 4
PP5UTB	GCGCTCTAGACCCAGCCGGACTCAGAATCTCCT	272	B	XbaI	5UT
3PP14B	TGCTTTCCCTGAGAAAGAT	273	B		Intron 4
5UTB39	AGCGGAATTCAGAGTCTCTCTCAGACGCG	274	B*39	EcoRI	5UT B39
5PKCE	GGCGGAATTCGGCCGCCACCATGCGGGTTCATGGCGCC	275	C	EcoRI	5UT
3PP14C	TTCTGCTTTCTTGAGAAAGAC	276	C		Intron 4
PP5UT	GGCGGAATTCGGACTCAGAAATCTCCCCAGACGCCGAG	277	B	EcoRI	5UT
PP3PEI	CCGCGAATTCATCTCAGGGTGAGGGGCT	278	A,B,C	EcoRI	Exon 4
PP3PEIH	CCGCAAGCTTTTCATCTCAGGGTGAGGGGCT	279	A,B,C	HindIII	Exon 4
3PEIHC7	CCGCAAGCTTTTCAGCTCAGGGTGAGGGGCT	280	Cw*07	HindIII	Exon 4



10022066 . 090902



10022066.090902

Primer Name	Sequence 5'-3'	SEQ ID NO:”
T7Prom	TAATACGACTCACTATAGGG	281
BGHrev	TAGAAGGCACAGTCGAGG	282
PPI2E2R	GTCGTGACCTGCGCCCC	283
PPI2E2F	TTTCATTTTCAGTTTAGGCCA	284
ABCI3E4F	GGTGTCTGTCCATTCTCA	285

5'CY5 Sequencing Primers

TABLE 18



TABLE A

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
6	398.2 (+3)	- - W D R H T X F	134
6	448.2 (+2)	- - - - - Y T	N/A
7	382.7 (+2)	V Q F E A A T	286
7	418.7 (+2)	A Q F A S G A G Z	135
7	455.2 (+2)	A L G A - - R G Y	287
7	489.1 (+2)	- - V - - G H X Y	288
7	506.8 (+2)	X S - - - C E Y	289
8	402.2 (+2)	- G - - C D Y	136
8	419.2 (+2)	G S H F G V A Y	137
8	433.8 (+2)	A P P P P P P P P	31
8	455.2 (+2)	- - - Z A R G Y	290
8	462.2 (+2)	D P H <u>A</u> <u>P</u> P Z Y	291
8	507.2 (+2)	A V P S X H X X Y	292
8	512.3 (+2)	X A Z V Z M T A Y	293
8	512.8 (+2)	A L N G <u>R</u> <u>V</u> <u>T</u> M Y	294
8	516.9 (+2)	N Q Z H G S A E Y	138
8	522.9 (+2)	F G <u>X</u> <u>A</u> <u>C</u> X A T S Y	295
8	642.7 (+2)	P M N D W X M T Z T Y	139
9	331.4 (+3)	A P M A R G Z Y	140
9	418.7 (+2)	F V S N H A Y	141
9	426.2 (+3)	- - - - - - - S Y	N/A
9	433.3 (+2)	N P P A Z Z P N	142
9	437.0 (+2)	T G - - - A Y	143
9	441.2 (+3)	- Q - D P P P D M Z Y	144
9	446.6 (+2)	G Q Z Z A V D F	145
9	453.6 (+2)	X Q - - A G G Z Y	296
9	465.2 (+2)	S Q F G G G S Q Y	146
9	476.2 (+2)	S Q F D H V T Y	147
9	481.0 (+2)	G Q H A S V X S Y	297
9	514.2 (+2)	- - A A H V P P G Y	298
9	550.2 (+2)	F M D V G A P T V Y	299
9	578.0 (+2)	T P X G E P Y Z S Y	148
10	398.3 (+2)	X A N - - V T	149
10	448.2 (+2)	A Q A A P F A G Y	300
10	448.4 (+2)	V V V F G V Z F	301
10	450.4 (+2)	A Q M - - S E Y	302
10	456.8 (+2)	C P L S C F T	150
10	464.7 (+2)	- - - - F G H Y	303
10	473.7 (+2)	<u>A</u> <u>L</u> W - - P Z F	304
10	486.4 (+2)	V P H Z N A Y	305



10022066.090902

TABLE A CONT'D.

10	498.7 (+2)	- - - - - G H G G Y	306
10	509.0 (+2)	F L Z A M Z S T Y	151
10	527.7 (+2)	G Q Y V <u>V</u> <u>Z</u> P T Y	307
10	532.0 (+2)	T V X D S Z T H Y	152
10	540.2 (+2)	P M F D P P Z T F	308
11	469.2 (+2)	A Q A E S L R Y	309
11	480.6 (+2)	X A V G H S G G T Y	310
11	511.2 (+2)	- - - - - P T Y	N/A
11	516.7 (+2)	E S X P N N V P Y	311
12	383.0 (+3)	L <u>A</u> <u>H</u> <u>T</u> <u>E</u> <u>C</u> P R G Y	312
12	435.0 (+2)	- - - - - P S Y	N/A
12	473.2 (+2)	<u>V</u> <u>Q</u> <u>G</u> P V G V Q Y	313
12	475.0 (+2)	R G X G V A G T A F	314
12	505.0 (+2)	T G A P V S E E G Y	315
12	513.7 (+2)	V Q X Y Y G <u>S</u> <u>V</u> V	316
12	519.0 (+2)	E P A M V X Z C F	317
12	531.2 (+2)	G Q P G A P X G G Z Y	318
12	541.0 (+2)	G P <u>P</u> <u>H</u> <u>N</u> G X R A Y	319
12	542.2 (+2)	A A H W H V E A Y	320
12	553.7 (+2)	T P P T R R E S Y	321
12	577.2 (+2)	F P T D R R S Q F	322
13	363.0 (+3)	Y T G V S Y X H F	323
13	447.0 (+2)	A Q A S A P D A Y	324
13	465.0 (+2)	V Q Y Y X P F	325
13	503.6 (+2)	G Q R K G A G S V F	153
13	553.2 (+2)	X Q Z X - - D V Y	326
13	590.8 (+2)	A T <u>G</u> <u>T</u> <u>A</u> <u>Z</u> N X N Z Y	327
14	460.7 (+2)	V V A P I T T G Y	154
14	471.5 (+2)	V V A C V - - - Y	155
14	495.2 (+2)	X Q Y T V G Y F	328
14	525.3 (+2)	P L A - N - H T Y	156
14	541.3 (+2)	P L F G Q T A G Q Y	329
14	550.4 (+2)	A - - - - Q X E Y	330
14	577.2 (+2)	Z G Y G N P X N G A Y	331
15	459.8 (+2)	V Q G P V G T D F	332
15	470.9 (+2)	V A G G W - - - F	333
15	514.2 (+2)	F Q A R X T E Y	157
15	536.6 (+2)	X A G F F X X E Y	334
15	544.2 (+2)	X Q - - - - Z Y	N/A
15	564.2 (+2)	S G A X D R A Y Z F	335
16	467.1 (+2)	F Q - - - - T X	N/A
16	500.4 (+2)	T P - - - - A Z A F	336
16	501.0 (+2)	V V A T Z N Z Z X	337
16	503.6 (+2)	Y M V T - - - F	338
16	517.4 (+2)	A L G S Z A X M P F	339
16	521.3 (+2)	A P A V - - - V G Y	340



TABLE A CONT'D.

		V G Y V D D T Q F	158
		- - - - - T G F	N/A
16	536.0 (+2)	P V P N V R X N Y	341
16	544.4 (+2)	- - - - - T X S X	N/A
16	557.6 (+2)	T L E G W M S Z Y	342
16	561.5 (+2)	Y M V C N A E E Y	343
16	596.7 (+2)	- - - - - X R D X Y	N/A
16	596.9 (+2)	S L X - - - - F	N/A
17	343.2 (+3)	A Q H P <u>S</u> <u>A</u> <u>X</u> <u>R</u> F	344
17	351.3 (+3)	A A F C G - - - X V	159
17	408.7 (+2)	Y L H - - E T	160
17	441.2 (+2)	- - - - - Z A Y	N/A
17	451.4 (+2)	I L G P P G S V Y	161
17	455.0 (+2)	G L G Z T S A E F	345
17	462.4 (+2)	X L G D V N M Y	162
17	483.8 (+2)	V M <u>G</u> <u>X</u> <u>T</u> <u>N</u> A N F	346
17	490.2 (+2)	N A X G R E S S F	347
17	497.2 (+2)	A M N P T N T V F	348
17	507.0 (+2)	- - - - - X V E F	N/A
17	511.2 (+2)	X Q A P A X F V Y	349
17	519.2 (+2)	T A R V X S V E Y	164
17	526.8 (+2)	A L F - - - F T Y	350
17	542.8 (+2)	X Q X N A Y X S Y	351
17	563.2 (+2)	G L A R <u>C</u> <u>S</u> Z V E Y	352
18	503.8 (+2)	S Q X <u>A</u> <u>A</u> <u>G</u> V D V F	353
18	511.7 (+2)	P Q G Z M A - - Y	354
18	519.6 (+2)	- V F V S H T T F	355
18	538.8 (+2)	<u>H</u> X T G <u>N</u> E A T S F	356
18	565.7 (+2)	A E <u>F</u> <u>W</u> A C Z X Y	165
18	566.2 (+2)	Y M I D P S G V S Y	166
18	581.2 (+2)	X Q G H H E M F Y	357
20	448.2 (+2)	A A G X G P T F Y	358
20	560.0 (+2)	X V E X T T D Y Y	167
20	614.0 (+2)	I A V G Y V D D T Q F	22
21	507.2 (+2)	V A <u>F</u> <u>V</u> <u>X</u> F V G Y	359
22	510.8 (+2)	<u>A</u> <u>L</u> M P - - X N Y	360
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F	361
24	546.3 (+2)	- - Z D R N V T F	362
25	546.3 (+2)	V V T M - - - Z Y	363

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.



10022066.090902

TABLE B

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
6	471.8 (+2)	A Z V E C E T Y	364
7	418.7 (+2)	A Q F A S G A G Z	365
7	504.2 (+2)	Z G X G G G P A T S Y	366
8	402.2 (+2)	- G - - C D Y	367
8	441.2 (+2)	- - - - - Z S F	N/A
8	516.9 (+2)	N Q Z H G S A E Y	368
9	331.4 (+3)	A P M A R G Z Y	369
9	349.4 (+3)	- - - - - G F Y	N/A
9	418.7 (+2)	A Z V N S G - Y	370
9	426.2 (+3)	A A S S Z V - - P P Z Y	371
9	433.3 (+2)	N P P A Z Z P N	372
9	437.0 (+2)	A C G G C G Z D Y	373
9	441.2 (+3)	- Z - D P P P D M Z Y	374
9	446.6 (+2)	G Q Z Z A V D F	375
9	578.0 (+2)	T P X G E P Y Z S Y	376
10	426.5 (+2)	G P - - - P Z Y	377
10	443.2 (+2)	A P Z Y P P P P	378
10	448.3 (+2)	G Z V C T P G S F	379
10	456.8 (+2)	C P L S C F T	380
10	464.7 (+2)	S Q F G G G S Q Y	381
10	465.4 (+2)	A S G F N G S Z Y	382
10	503.8 (+2)	- Z - - Y T A Y	383
10	508.7 (+2)	G Z P P H N G F Y	384
10	517.0 (+2)	I K A D H V S T Y	385
10	527.7 (+2)	X Z A D H V X P Y	386
10	540.2 (+2)	- - - - P G Z V Y	387
10	549.2 (+2)	Z S V - - - Z T G Y	388
11	437.0 (+2)	H X G N Q A A Y	389
11	511.4 (+2)	Z A G T T V P V S Y	390
11	527.4 (+2)	G Q Y P T Q P T Y	391
11	581.4 (+2)	F A G S Z S N T S T Y	392
12	494.8 (+2)	S Z G G - - - T G Y	393
12	526.8 (+2)	Z G P P N Y X T Y	394
12	547.1 (+2)	V K V I Q Q E S Y	395
13	454.6 (+2)	L P P P P P P P P	396
13	476.0 (+2)	A K Y S T P A T L	397
13	503.6 (+2)	G Q R K G A G S V F	398
13	513.1 (+2)	R Z S A N H E A X	399
13	526.4 (+2)	G K V R T D I T Y	400
13	553.2 (+2)	V V X P A V R S T Y	401



TABLE B CONT'D.

13	561.0 (+2)	A K Y P H V E D Y	402
13	571.3 (+2)	A Z N X S A Y V X Y	403
13	601.2 (+2)	E V V G D T Z Y	404
14	438.2 (+2)	A K A G I T T T L	405
14	490.8 (+2)	V - - T Z A G S A F	406
14	517.2 (+2)	A Z A A A N V X X Y	407
14	531.5 (+2)	A N H S V R D T Y	408
14	535.3 (+2)	E - - - G X R Z Y	409
14	552.8 (+2)	X Z H N D Z S T Y	410
14	577.2 (+2)	A N E Z X G - - - Y	411
15	497.3 (+2)	A A G P T A Z E S Y	412
15	514.2 (+2)	V A G X V F M Z Y	413
15	527.0 (+2)	A Z Y Z A Z V V F	414
15	564.2 (+2)	A Z F - - - Z X Y	415
15	577.2 (+2)	Z G Y G N P X N Z Y	416
15	626.0 (+2)	- - - - - Z A P C H Y	417
16	521.6 (+2)	A H A V Q R V V Y	418
16	525.6 (+2)	T Z X T V V X N Y	419
17	446.8 (+2)	A Z Z A S G X A F	420
17	492.8 (+2)	G S H S M R Y F	421
17	503.8 (+2)	Y G Y G A T V E F	422
17	967.6 (+1)	V Z - - - T T F	423
18	451.4 (+2)	Q P G P Q I V Y	424
18	455.2 (+2)	N G Z X S N N Y	425
18	475.2 (+2)	A N X V Z X E Y	426
18	489.1 (+2)	G Z - - - Z G X X Y	427
18	497.8 (+2)	A M N P T N T V F	428
18	525.2 (+2)	Y N - - - Z X F	429
18	538.8 (+2)	- M - - S Y Z N F	430
18	565.7 (+2)	A E <u>F</u> <u>W</u> A C Z X Y	431
19	521.6 (+2)	S Z F G <u>C</u> <u>P</u> T R F	432
19	524.6 (+2)	X G A X S N - - E F	433
19	571.2 (+2)	R Z A A Y R X T Y	434
19	646.2 (+2)	T N X H D G D G A T Z Y	435

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.



10022066 .090902

TABLE C

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
6	398.2 (+3)	- - W D R H T X F	436
6	448.2 (+2)	- - - - - Y T	N/A
8	419.2 (+2)	G S H F G V A Y	437
8	441.2 (+2)	V P <u>C</u> <u>G</u> <u>Z</u> <u>Z</u> S Y	438
8	473.2 (+2)	T A Z X H R G Y	439
8	512.8 (+2)	X A Z Y E H T Y	440
8	516.9 (+2)	N Q Z H G S A E Y	441
8	546.8 (+2)	N G <u>X</u> <u>A</u> <u>M</u> <u>H</u> W T Y	442
9	418.7 (+2)	F V S N H A Y	443
9	437.0 (+2)	T G - - - - A Y	444
9	465.2 (+2)	S Q F G G G S Q Y	445
9	476.2 (+2)	S Q F D H V T Y	446
9	481.0 (+2)	- P - - G Z D E V	447
9	514.2 (+2)	N G Y D G P N A G Y	448
9	578.0 (+2)	T P X G E P Y Z S Y	449
10	398.3 (+2)	X A N - - V T	450
10	448.3 (+2)	M P H S G Y G F	451
10	450.4 (+2)	V D X - - - Y	N/A
10	456.8 (+2)	C P L S C F T	452
10	464.7 (+2)	- - - - - P G F Y	453
10	486.2 (+2)	- A - P H P M G Y	454
10	494.2 (+2)	A Q T V G Y G E Y	455
10	508.7 (+2)	- - - - - S V Y	N/A
10	509.0 (+2)	F L Z A M Z S T Y	456
10	532.0 (+2)	T V X D S Z T H Y	457
11	444.1 (+2)	T P - - A R A P T	458
11	469.2 (+2)	S E H D R M Y	459
11	480.6 (+2)	T G N C S G T G T Y	460
11	496.8 (+2)	A Q V N P S X T Y	461
11	532.3 (+2)	S P G A E T R A X Y	462
12	473.2 (+2)	Y L G - - - G A F	463
12	494.8 (+2)	X T S F M Z V Y	464
12	499.0 (+2)	- P - - - P S S G Y	465
12	505.0 (+2)	T P - - - G R M Y	466
12	513.7 (+2)	P M F D Z Z V Y	467
12	519.0 (+2)	Y L - - - R T F	468
12	531.2 (+2)	A Q E H G C A A Z F	469
12	542.2 (+2)	- <u>M</u> - - - <u>G</u> <u>V</u> H D Y	470
12	550.2 (+2)	Y V S - - R N Q Y	471
12	553.7 (+2)	A Q Y A A G E S F Y	472



TABLE C CONT'D.

12	564.0 (+2)	T P H T Z H D E Y	473
12	565.2 (+2)	Y M - - - F M Y	474
13	396.1 (+3)	D P H Y V S G H Z F	475
13	401.2 (+2)	M V G X X P A T	476
13	526.4 (+2)	Z A S P G E X T S Y	477
14	460.7 (+2)	V V A P I T T G Y	478
14	471.5 (+2)	V V A C V - - - Y	479
14	525.3 (+2)	P L A - N - H T Y	480
14	543.2 (+2)	X A X Y R R M Y	481
14	550.4 (+2)	P L A M Z X Y T Y	482
15	460.6 (+2)	- P - M P G X A Y	483
15	461.0 (+2)	H T T S Z N A Y	484
15	506.0 (+2)	M A A M V G V A V Y	485
15	508.4 (+2)	G P Z V M Z H G Y	486
15	514.2 (+2)	F Q A R X T E Y	487
15	520.0 (+2)	L P H Q P L A T Y	488
15	525.2 (+2)	A A A X V - - - V T Y	489
15	536.6 (+2)	X P E M G Z F S Y	490
15	544.2 (+2)	Y V - - V R - V F	491
15	564.2 (+2)	F V T X N X E E Y	492
16	489.0 (+2)	A A P V G A X E S Y	493
16	500.4 (+2)	G S - - - S Y T Y	494
16	522.0 (+2)	V G Y V D D T Q F	21
16	525.7 (+2)	Y V A - - - P A F	495
16	533.0 (+2)	V G Y - - A H P G F	496
16	535.7 (+2)	Z A T N S V T S T Y	497
16	537.0 (+2)	- - - - - S T Y	498
16	545.8 (+2)	Y A T A G E M M A F	499
16	547.0 (+2)	S P T Y T H A V A F	500
16	557.0 (+2)	M P A - - M V M A F	501
17	351.3 (+3)	A A F C G - - - X V	502
17	393.7 (+2)	S P N E D X M Z V F	503
17	403.2 (+2)	V A A T A G A V F	504
17	408.7 (+2)	Y L H - - E T	505
17	414.8 (+2)	T A F P F V F	506
17	451.4 (+2)	I L G P P G S V Y	507
17	462.4 (+2)	X L G D V N M Y	508
17	476.2 (+2)	Y G - - - V X S M	509
17	490.8 (+2)	X P H C S C S S F	510
17	504.0 (+2)	D P P C W G V S F	511
17	507.0 (+2)	- - - - X V E F	N/A
17	511.2 (+2)	- - - - A H D A Y	512
17	519.2 (+2)	T A R V X S V E Y	513
17	526.8 (+2)	X S D G R Z X T Y	514
17	542.8 (+2)	N M N D L V S E Y	515
17	557.2 (+2)	M P A A D Y E V A F	516
18	474.8 (+2)	A E I L Q V I Y	517
18	503.8 (+2)	A P - - - X V S Y	518



TABLE C CONT'D.

18	514.7 (+2)	M P A G Y N N V Y	519
18	519.6 (+2)	Y M S G <u>X</u> <u>Y</u> <u>G</u> T F	520
18	526.8 (+2)	- - - <u>A</u> <u>V</u> V A Z S Y	521
18	538.8 (+2)	X P V V P A A Z T Y	522
18	566.2 (+2)	Y M I D P S G V S Y	523
18	616.3 (+2)	F A N G V <u>Z</u> <u>G</u> <u>C</u> <u>A</u> <u>F</u> A F	524

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.



TABLE D

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
6	493.0 (+2)	N H A V G - - V S M	525
6	557.8 (+2)	H N V F Z P T S N A	526
7	434.8 (+2)	S V C E T E S X	527
7	481.3 (+2)	T H P S Z A C A F	528
7	489.1 (+2)	- H - - S P X X	N/A
8	420.1 (+2)	A N X E G P H T	530
8	441.7 (+2)	G H S P P T S S L	531
8	494.8 (+2)	C H S A F A L	532
8	511.6 (+2)	H H A F A Z V X V	533
8	519.4 (+2)	D H Y Y X A G S X	534
9	411.4 (+2)	E X A P H A A X	535
9	424.3 (+2)	A A A X R C E X	536
9	426.1 (+2)	G H Z A P A A S X	537
9	441.7 (+2)	V H N P Z S S X	538
9	444.2 (+2)	A G G P T X C R X	539
9	455.5 (+2)	L H L L T L E A	540
9	490.3 (+2)	A G G Z P A T P P A X	107
9	513.1 (+2)	S H Z G C V Z P A V	108
9	520.0 (+2)	X H R L C S P T X	541
10	404.2 (+2)	S V S X P H A P	542
10	417.1 (+2)	A P F T G G N G X	543
10	433.8 (+2)	G H D P D S P A A	109
10	446.2 (+2)	E H G X E N G H	544
10	455.4 (+2)	E H V A S S P A L	110
10	460.4 (+2)	H H A P C G V S X	545
10	464.0 (+2)	N H A I V S T S V	546
10	464.7 (+2)	G H Z N S V T S V	547
10	465.3 (+2)	S H Z A P C T S V	548
10	469.4 (+2)	F V A R F V S X	549
10	469.6 (+2)	H H S D G S V S L	550
10	473.7 (+2)	S H A G A P P P T X	551
10	482.6 (+2)	M C Z - G M P A X	111
10	482.8 (+2)	G H G A N N D P A X	112
10	495.7 (+2)	X H S Z P A G P A X	113
10	508.3 (+2)	X H V V S - - V X	552
10	511.2 (+2)	A V X D C C Z V A V	553
10	522.3 (+2)	E X G G N T N P Z X	554
10	522.7 (+2)	Y H G S Z N P E X	555
10	569.6 (+2)	- - - - - T Y S Y	556
10	574.3 (+2)	- - - - - - - M	N/A



10022066 .090902

**TABLE D
CONT'D.**

11	405.7 (+2)	S H - - - Y F	557
11	425.8 (+2)	A H P D Z A X V	558
11	444.7 (+2)	G T A H Y Z V X	559
11	448.9 (+2)	M H A D N P V X	114
11	455.7 (+2)	S H <u>V</u> <u>D</u> <u>R</u> P S X	560
11	459.7 (+2)	T G A A F Z N P X	561
11	482.8 (+2)	G H <u>C</u> <u>P</u> R N P A X	115
11	495.7 (+2)	X H S G A P Z A P X	116
11	516.7 (+2)	X H D <u>T</u> <u>E</u> <u>H</u> <u>A</u> P X	117
11	562.3 (+2)	- - - Y Z A Y V Y	562
12	411.7 (+2)	G H G P T X A A V	563
12	428.8 (+2)	V P - - - - -	N/A
12	444.7 (+2)	Y Q H T G A V L	564
12	448.4 (+2)	T Q A P G N P V L	118
12	460.3 (+2)	T Z A <u>G</u> <u>C</u> <u>M</u> <u>V</u> P X	119
12	490.9 (+2)	T H T Q P G V Q L	565
12	507.4 (+2)	G H A G H V P P E X	566
12	511.6 (+2)	T H F R Y V S X	567
12	528.1 (+2)	E H R P D R V F	568
13	427.6 (+2)	S H A Q T V V L	569
13	449.2 (+2)	S H A N S A V V L	570
13	464.8 (+2)	M V - - H P V X	120
13	487.6 (+2)	Y H H G G V S A F	571
13	506.2 (+2)	- H - - G H T G Y X	572
14	420.1 (+2)	N H A N G L T L	573
14	438.7 (+2)	- - - - - P X X	N/A
14	456.7 (+2)	A H S V P S P A F	121
14	477.7 (+2)	M H T - - P A P V	122
14	482.8 (+2)	P G A A V V P S X	123
14	560.8 (+2)	G H A G M G C V F Z X	574
14	592.3 (+2)	M R - - - - G X E X	575
15	418.9 (+2)	S H G V P R A X	576
15	439.0 (+2)	E H H M P X X	577
15	454.3 (+2)	H H Z C A A G A X	578
15	492.1 (+2)	X V D <u>Z</u> <u>A</u> <u>E</u> P X V	579
15	510.1 (+2)	I H T P E N P V I	124
15	520.0 (+2)	M G X P V R H M V	580
15	524.2 (+2)	S H Y D W Z V X	581
15	532.9 (+2)	M P H S H P F V X	582
15	577.2 (+2)	Z C V R C Z N G V F	583
16	412.9 (+2)	S H A G A G X V X	584
16	418.3 (+2)	G H X E G P X X	585
16	424.3 (+2)	X H G G D H V X	586
16	448.6 (+2)	E Z A H S X V X	587
16	448.9 (+2)	Y H H D X V X	588
16	454.3 (+2)	M A G A W C R X	589
16	456.7 (+2)	S H <u>D</u> <u>G</u> <u>S</u> V P T X	125
16	464.2 (+2)	F H - - X X X	N/A



TABLE D CONT'D.

16	469.9 (+2)	E H - - - T V X	590
16	472.3 (+2)	M A X - - - V V	591
16	499.0 (+2)	G H A <u>X</u> T D G X T X	592
16	504.1 (+2)	P V <u>S</u> <u>H</u> <u>X</u> V N E L	593
16	507.7 (+2)	X X Y T <u>P</u> <u>G</u> H T X	594
16	522.7 (+2)	- - - - - P V X	N/A
16	523.3 (+2)	M A H S - - P V F	127
16	529.9 (+2)	X H Y D R N Q X	595
16	536.2 (+2)	E A - - C Z V T T Y	596
16	547.9 (+2)	- - - - - A X S V	N/A
16	552.4 (+2)	X Z <u>A</u> <u>P</u> <u>T</u> S V F Z X	597
17	367.7 (+3)	<u>F</u> <u>T</u> <u>M</u> <u>P</u> A H P S T X	598
17	490.8 (+2)	M T X G Y G E P X	599
17	557.3 (+2)	A H G R K M S K S L	600
17	340.7 (+3)	- <u>H</u> - - H A Z V X	601
17	367.7 (+3)	- - - - R X S H X	N/A
17	419.8 (+2)	- - - H A V G X X	602
17	462.8 (+2)	M S S N E X X M	603
17	476.2 (+2)	G H - - - P C C	604
17	504.2 (+2)	X H V X A V N E X	605
17	523.2 (+2)	- H - - - - P V F	128
17	543.2 (+2)	X H E V Z P H X X	606
17	590.2 (+2)	A T E H <u>C</u> <u>F</u> <u>V</u> M E X	607
18	456.4 (+2)	A H S N L A S V L	608
18	463.3 (+2)	V X A P A N D X X	609
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X	129
18	491.2 (+2)	V H T C V N P V X	130
18	497.8 (+2)	S H Q R Q L L L	610
18	515.8 (+2)	E W <u>H</u> <u>Y</u> P V S X	131
18	519.7 (+2)	<u>F</u> <u>H</u> <u>M</u> <u>D</u> X Z T F	611
18	543.4 (+2)	X H E <u>V</u> <u>Z</u> P H X X	612
18	596.8 (+2)	<u>F</u> <u>H</u> <u>H</u> <u>T</u> Z S N P X X	613
19	434.6 (+2)	- H <u>G</u> <u>C</u> <u>P</u> G M P X	614
19	496.6 (+2)	<u>E</u> <u>T</u> <u>P</u> <u>E</u> H A P V X	132
19	539.6 (+2)	<u>M</u> <u>X</u> P G N S A X Y X	615

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.



101 0066.090902

TABLE E

fraction	ion for MS/MS	derived peptide sequence	SEQ ID NO:
7	504.1 (+2)	H M S G Z P T S Y	65
7	549.2 (+2)	H N Z A A H Z E Y	66
8	517.0 (+2)	N Q Z H G S A E Y	616
8	526.0 (+2)	H A A <u>X</u> <u>Y</u> <u>S</u> Z V Y	67
8	642.7 (+2)	P M N D W X M T Z T Y	617
10	465.3 (+2)	S Q F G G G S Q Y	618
10	484.3 (+2)	Y Q S <u>D</u> <u>H</u> R Y	68
10	509.0 (+2)	F L Z A M Z S T Y	619
10	532.0 (+2)	T V X D S Z T H Y	620
11	424.3 (+2)	H X S T Z D F	69
11	464.3 (+2)	H A P P T D P P P	70
11	550.0 (+2)	H G P A N R <u>D</u> S V F	71
11	563.3 (+2)	F P Y P T D P Z Y	72
12	531.2 (+2)	K N A N L V Q L Y	621
14	585.6 (+2)	R S F X X E N E Y	74
16	488.7 (+2)	H M Z N P T S Y	75
16	661.9 (+2)	Y V X F - - - V Y	76
17	577.6 (+2)	R S M X R <u>C</u> P E Y	77
18	451.1 (+2)	I L G P P G S V Y	622
18	523.0 (+2)	- - <u>F</u> <u>V</u> <u>T</u> A Z T Y	78
19	565.6 (+2)	Y M I D P S G V S Y	623
19	503.8 (+2)	S Q X A A G V D V F	624
20	560.0 (+2)	X V E X T T D Y Y	625
20	582.4 (+2)	M Y N <u>C</u> <u>N</u> E X D Y	79
21	448.2 (+2)	A A G X G P T F Y	626
21	614.0 (+2)	I A V G Y V D D T Q F	22
22	507.2 (+2)	V A <u>F</u> <u>V</u> <u>X</u> F V G Y	627
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F	628
23	510.8 (+2)	<u>A</u> <u>L</u> M P - - X N Y	629
25	562.8 (+2)	N Q F Q A L L Q Y	80

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.